

APPLICATION
FOR
UNITED STATES LETTERS PATENT

Entitled:

A METHOD AND DEVICE FOR IMPROVING PROTEIN STABILITY AND
SOLUBILITY

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Express Mail Label No.: EL835814020US

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Government Interests

Part of this invention was made with government support under GM59535-01 awarded by the National Institute of Health under the Small Business Innovative Research (SBIR) Program. The U.S. Government has certain rights in this invention

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Field of Invention

This present invention relates to a method and a device for improving protein folding, solubility, and stability when the protein is produced *in vivo* and *in vitro*.

15 Background of Invention

High throughput screening (HTS) of protein targets for drug discovery is a very costly process. On average it cost about \$100 million dollars to develop one drug and only three percent of the drugs make it through phase I clinical trials. About 5-15% of all proteins targets that are chosen for HTS never make it into the pipeline because the proteins are either insoluble, inactive, or unstable (sensitive to proteolysis). Although yeast and baculovirus systems for gene expression are often used as reliable alternatives, bacterial expression systems are still the main method of choice for over expressing recombinant proteins for drug development studies.

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Protein insolubility is one of the major problems associated with over-expressing proteins in bacteria. Protein solubility is judged empirically by assaying the levels of recombinant protein in the supernatant and pellet of lysed protein extracts. In general, small proteins (> 30kD) that are simple monomeric proteins can be found in the soluble fractions of bacterial extracts. In contrasts, proteins (<30 kD) or proteins that have complex secondary or tertiary structures are typically insoluble and are predominantly found in inclusion bodies. Although insoluble proteins can be denatured in urea and refolded *in situ*, full activity frequently is not restored.

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Yet another problem associated with the recombinant expression of proteins is proteolysis *in vivo*. Although a number of proteases have been removed by gene knock out technologies to reduce proteolysis in bacterial expression systems (such as lon in BL21 DE3), many proteins are very sensitive to endogenous bacterial proteases. Sensitivity to proteases can dramatically reduce the yield of full-length recombinant proteins. In extreme cases the expression of recombinant proteins is nearly undetectable due to proteolysis.

10 Object of the Invention

It is an object of the present invention to provide a method for expressing insoluble proteins

It is an object of the present invention to provide a method for expressing proteins that are sensitive to proteolysis.

It is an object of the present invention to provide a method for removing protease from protein extracts.

It is an object of the present invention to provide a method for using p26, SicA, and alpha crystallin type proteins in biochemical assays to remove non-specific protein interactions.

Summary

The present invention provides a method and a device for improving target protein folding, solubility, and stability when the target protein is produced *in vivo* and *in vitro*. In one embodiment, the present invention provides a method for expressing target proteins in a plasmid system as a fusion (chimera) having a domain of p26, SicA, or alpha crystallin type proteins to improve the target protein stability and solubility when the target protein is over expressed in bacteria such as *E. coli*. The method comprises inserting a gene coding for a target protein into a multiple cloning site (MCS) of a vector system, proximal to and just downstream of the p26, SicA or alpha crystallin type protein

coding site or domain that is adjacent to a thrombin cleavage site and then expressing the target protein. Preferably, the target protein when expressed in the absence of the inventive vector construct is insoluble and accumulates in inclusion bodies in the cells. Target protein expression in the inventive vector system is driven for example by a strong bacterial promoter such as (TAC). Other strong promoters would give comparable results. The expression is induced for example by the addition of 1mM Isopropyl β -D-Thiogalactopyranoside (IPTG) that de-represses the lac repressor protein (lac I^q). The method includes purifying the target protein produced by the expression system. In one embodiment, the soluble recombinant target protein is purified for example using a fusion tag (polyhistidine; Hoffman La Roche; Basel, Switzerland) Further, the p26, SicA, or alpha-crystallin type protein domain can be removed by thrombin cleavage.

In another aspect of the present invention, a device that acts as a pre-column filter for reducing unwanted proteolysis on a chromatography column during purification of a target protein is provided. The pre-column filter is an affinity chromatography resin useful for removing proteases from crude protein extracts. In one embodiment, the pre-column filter comprises bovine lens alpha crystallin coupled to CNBr-sepharose.

The vector comprises the active anti-parallel beta sheets and the active charged core domain of p26, a small molecular chaperone/ α -crystallin type protein from the brine shrimp *Artemia*. When this active domain of p26 is fused to a gene target, the recombinant expression of that gene target produces soluble recombinant target proteins. As used herein "charged core domain" is defined as the amino acid residues 160-192. As used herein the active anti-parallel beta sheets is defined by amino acid residues 36-160. As used herein the term "otherwise insoluble protein" is defined as a protein that is insoluble when expressed in a prior art vector system such as the pET28a over-expression vector; trademarked Kan (Novagen, Inc., Carlsbad, CA). Examples of otherwise insoluble proteins expressed in *E. coli* include pepsinogen, and procathepsin D.

As used herein, the term "fusion tag" or "protein fusion" is defined as a DNA molecule that is added to a gene that is expressed in frame thereby making a protein chimera. Examples of suitable fusion tags include but are not meant to be limited to: polyhistidine; glutathione; maltose binding protein; S protein; and beta-galactosidase.

The target gene for the otherwise insoluble protein is inserted in frame into the poly-linker region of the vector plasmid just downstream of the beta-core domain of p26 (Vector S) or the entire alpha-A-crystallin (Vector AP). A thrombin cleavage site provides for a removable fusion tag.

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VECTOR-S (S = soluble)	Fusion domain p26 or SicA
VECTOR -AP (AP = anti- proteolysis)	Fusion domain of α -A crystallin

Unexpectedly, alpha-A-crystallin, but not p26 or SicA is shown to result in a reduction in unwanted proteolysis.

10 **Brief Description of the Drawings**

FIG. 1. shows a plasmid map for the Vector System DNA construct.

FIG. 2. is a representation of a pre-column filter placed in series with a resolving column such as a gel filtration or an ion exchange column.

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FIG. 3 is a digital image of an SDS PAGE gel showing purified BC-pepsinogen.

FIG. 4 shows a digital image of a 12% SDS PAGE gel of p26 protein purified by nickel affinity chromatography resin. Because p26 is a multi-oligomer, it has a tendency to elute over several fractions, even when a sharp gradient is provided. Fractions identified using the SDS gel and containing p26 are dialyzed into Pipes magnesium buffer (20 mM Pipes pH 7.0, 1mM MgCl₂). Following dialysis the target protein was stored at -20°C and used in less than 1 week for kinetic assays and chromatography experiments.

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25 FIG. 5A shows the chromatograph of purified α -crystallin.

FIG. 5B provides a digital image of an SDS PAGE gel of purified α -crystallin.

FIG. 6 provides a graph that shows the inhibition of elastase activity with α -crystallin. Elastase activity was measured using a para-nitroaniline substrate obtained from

Calbiochem (La Jolla, CA). Assays were performed with a Benchmark microplate reader (Bio-Rad). Elastase was purchased from either Sigma or Calbiochem. In a 100 μ l assay 50 μ g of peptide substrate, 1 μ g of elastase, and 50-100 μ g of either uncoupled p26, α -crystallin conjugated sepharose, BSA conjugated sepharose, or buffer (negative control) was used.

FIG. 7 is a graph that illustrates the NaCl dependency of α -crystallin in inhibiting elastase activity. One μ g of elastase was incubated with 5 μ l of α -crystallin conjugated sepharose in the presence of 0-200 mM NaCl. Increasing the NaCl concentration reduced the ability of α -crystallin to inhibit elastase activity.

Detailed Description of the Invention

Referring to FIG. 1, an expression vector consisting of a gene fusion between an unstable or insoluble protein could be stabilized or protected from proteolysis with the appropriate class of small molecular chaperone/ α crystallin type proteins such as p26 from *Artemia*, SicA from *Salmonella* and α -A-crystallin protein from bovine lens. Unexpectedly it was shown that the protein p26 from *Artemia* has an active domain that can assist in the formation of soluble proteins based on its properties as an α -crystallin type protein. It was determined that full-length p26 protein is completely insoluble when expressed in *E. coli* at 37-C. It is expected that proteins with a similar structural fold such as the SicA protein from *Salmonella typhimurium* could be substituted for p26. These results indicate that p26 and SicA are functionally very similar. It is also envisioned that the chaperone could be co-expressed on two different promoters either on the same plasmid or on different plasmids in the bacteria. The advantages of co-expression are that it would not require the removal of a fusion tag (such as thrombin) prior to purifying the protein of interest.

Here it is demonstrated that not all α -crystallin type proteins are identical. In particular, bovine lens α -A-crystallin but not the p26 protein from *Artemia* or the SicA protein from *Salmonella typhimurium* was shown to specifically inhibit proteases. By expressing α -A-crystallin in *E. coli* it would be possible to stabilize normally unstable recombinant proteins. By providing a means to protect recombinant proteins

from unfavorable proteolysis in vivo, it would be possible to develop many targets that were previously dropped from high throughput screening (HTS) programs.

Referring now to FIG. 2, One mg of bovine lens alpha crystallin is coupled per ml of CNBr-Sepharose (Lot# 276930, cat # 17-0430-01, Amersham Pharmacia Biotech) at 4°C for overnight. Following blocking for 1 hr with 100 mM Tris, the resin is introduced into a column. If the resolving column is gel filtration, the pre-column filter remains in series throughout the entire run. For ion exchange, the pre-column filter is removed just after loading the protein sample on the column. The pre-column filter removes unwanted proteases thereby improving the purity and yield of purified proteins. Optimal conditions for the buffer are pH 7-8 and low ionic strength (<100 mM salt, NaCl or KCl).

When lens alpha-A-crystallin was coupled to chromatography resins, it was determined that it was effective in killing 85% of elastase. One ml of alpha-A-crystallin protein (at 1mg/ml) was coupled to 100 µl swollen cyanogen bromide activated (CNBr) sepharose 4B resin according to Amersham Pharmacia (Piscataway, NJ). Briefly, CNBr powder was swollen in 1mM HCl, then washed with 1 mM HCl. Purified alpha-A-crystallin was dialyzed overnight into coupling buffer (0.1 M NaHCO₃, pH 8.3, 500 mM NaCl), with 50% glycerol. One ml of protein was added per 100 µl resin and coupled overnight at 4°C with shaking. Five volumes of coupling buffer was used to rinse away excess protein, and the resin was then blocked with 0.1 M Tris pH 8.0 for 2 hrs at room temp. The resin was then ready for use. Other types of resins that may also work include N-hydroxysuccinimide-activated (NHS) sepharose, aldehyde-agarose, 6-aminohexanoic acid matrices, and epoxy-activated matrices. Our findings indicate that a brief acid wash (pH 2.5) would remove the bound proteases thereby rejuvenating the resin.

Bovine α-crystallin and P26 from the brine shrimp *Artemia* have strong sequence identity and represent similar structural domains or folds (secondary structure). In particular, the most striking feature is the ~10 pleated beta sheets that are responsible for the oligomerization of this class of proteins. The oligomerization of alpha crystallin type proteins is thought to be necessary for the molecular chaperone activity. Unexpectedly, it was discovered that the first five anti-parallel beta sheets of p26 (amino acid residues 35-95) are sufficient for molecular chaperone activity. However, addition of the charged c-terminal core of p26 to the vector system improves the effectiveness of the chaperone

activity probably by stabilizing the oligomerization process or improving the solubility of the oligomers. SicA was cloned from *Salmonella typhimurium* and the gene was inserted into an expression vector. The α -A-crystallin gene was cloned from neonate bovine lens and inserted into an expression vector. Two clones of the entire p26 gene were used (p26-pRSET C, p26-pET21 from Tom MacRae of Dalhousie University (Halifax, Nova Scotia)). In addition to these full-length constructs, the entire p26 gene and three smaller domains were amplified by polymerase chain reaction for fusion expression studies. The entire p26 gene was cloned into the inventive expression vector. The inventive vector system contains the p15a origin of replication for co-expression studies. However, other origins can be used such as, for example, a ColE1 origin derived from pBR322. The p26 fusion domains were designed with an Nde I site at the carboxy terminus of p26 so that insoluble target proteins can easily be placed downstream. The vector construction is described in more detail in the next paragraph. Pepsinogen was used as a test target protein for the co-expression studies because it was shown to be completely insoluble when expressed in *E. coli* (Sachdev et al. 1998).

Vector Construction

The initial step in the vector construction was to replace the MCS found in the pKK223-3 vector with a newly constructed MCS. The new MCS knocked out the EcoRI site at base position 4584 and placed it further downstream in the new MCS (see FIG 1). The first restriction site found in the new MCS is an NdeI site which will be used for future in frame cloning. The vector contains pACYC184 as the vector backbone. A portion of the tetracycline gene in pACYC184 was deleted (BamHI to NruI) and replaced with the tac promoter, a newly constructed MCS, and the rmb ribosomal terminator (from the pKK223-3 vector, BamHI to ScaI). The inventive MCS had the following sequence:

CATATGGCTGCAGATCGCCCGGGCTCGAGGAGCTCGAATTC (SEQ. 1)

The p26 betacore domain was amplified using a forward primer containing an AseI site and a reverse primer containing the thrombin cleavage site as well as an NdeI

site. The p26 betacore cloning strategy was designed to knockout the NdeI site upstream of the betacore domain and place it downstream of the thrombin cleavage site. Allowing for future cloning of insoluble proteins downstream of the p26 betacore domain. The lac I^q gene was cloned into the AhdI-DrdI site of the vector. The lacI^q gene was PCR amplified from the *E. coli* strain MG1655. The forward primer contained an AhdI site and the reverse primer contained a DrdI site. The final vector size after all inserts were made is ~5.85Kb.

Materials used in Vector Construction

MG1655 kind gift from Terri Kenney of Genome Therapeutics (Waltham, MA)
P26 pRSETC kind gift from Tom MacRae
PKK223-3 Vector Amersham Pharmacia cat.# 27-4935-01 lot# 8054935011
pACYC184 NEB cat.# 401M
Bio-Rad quantum prep plasmid midiprep kit cat.# 732-6120
Qiagen qiafilter plasmid midiprep kit cat.#12243
lot#AMG006/BQ1069/G01/128
Oligonucleotides for MCS Oligo1: BRL# M4469B07 Oligo2: BRL# M4469B08
Oligonucleotides for p26 betacore amplifications NdeKOfor2, BRL# M9153B05
Thrombin Rev. BRL# M8902D08
Oligonucleotides for α -A- crystallin amplifications alpha-a BRL#10336-022
alpha-a rev BRL# N2571D10.
Oligonucleotides for SicA amplification SicAFor: BRL# N5263G12 and SicA
Rev: BRL# N5263h01.
Primers for lacI^q: lacI for. BRL#N2757F05 lacI rev2 BRL#N3305D03
Qiagen Qiaquick PCR Purification Kit cat.# 28104 Lot#BYG015/G01/178
Qiagen Qiaprep Spin Miniprep Kit cat.#27104 lot# BXG038/G03/318
Taq DNA Polymerase BRL cat.#10342-020 lot#1059060

Referring to FIG. 3 a 1L culture of BL21(DE3) cells containing betacore-pepsinogen was induced with 1 mM IPTG for 4 hours. The cells were centrifuged and lysed by sonication. The lysate was clarified by centrifugation, 0.2 μ m filtered, and loaded onto the 1.6 ml affinity column. The BC-pepsinogen protein was eluted with a linear gradient of NaCl (0-1M). The lane order was: 1 protein standard, 2, column load, 3, flow through, 4-7 fractions from NaCl gradient. Fraction 5 contained the purified BC-pepsinogen chimeric protein. Fusion of target genes coding for insoluble proteins to the beta pleated sheet and charged core domain of p26 improves the solubility of these proteins (FIG 3). It is envisioned that the inventive vector system will be very useful for improving the solubility of normally insoluble proteins such as for example immunoglobulin domains, proteases, cytokines, release factors and insoluble antigens.

Method for the Purification of p26

The entire p26 protein was expressed by growing *E. coli* to an optical density of about 1.0 and then inducing 4 hours with 1 mM IPTG. P26 protein was purified with Ni²⁺-NTA sepharose (Qiagen, cat #30410,) using the detergent HECAMEG (Calbiochem, cat# 373272, lot# b27260) to gently strip the protein contaminants that are nonspecifically bound to the p26 in the crude extract. At 37°C, all of the protein is in inclusion bodies, thus, an inclusion body prep was used to purify the protein. Briefly, following lysis by 3 x 15 sec bursts of sonication, the cell extract is centrifuged at 13 k RPM for 15 minutes. The pellet was resuspended in low buffer (10 mM Tris pH 8.0, 500 mM NaCl) with 0.1% detergent (HECAMEG) with protease inhibitors (1.5 μ g/ml aprotinin, 1.5 μ g/ml leupeptin, 1.0 μ M pepstatin, 0.2 μ M PMSF). The insoluble protein was recentrifuged and the pellet was resuspended in low buffer with 1% detergent. After centrifuging the sample one time, the pellet was resuspended in 8 M Urea. Low ionic strength buffer is used to bring the solution to 4 M urea, the sample was centrifuged again, and the supernatant was filtered through a 0.2 μ m filter and loaded onto a nickel sepharose column. After loading the column, the p26 was refolded with a linear reverse gradient of Urea (4-0 M Urea in low buffer). The protein bound to the column is washed with a 0.1% detergent to remove protein contaminants and the p26 is eluted with a linear

gradient of high Imidazole buffer (10 mM Tris, 500 mM NaCl, 250 mM Imidazole). The protein fractions were run on a 12% SDS-PAGE gel to determine which fractions were to be pooled. FIG. 4 shows a digital image of a 12% SDS PAGE gel of p26 protein purified by nickel affinity chromatography resin. Because p26 is a multi-oligomer, it has a tendency to elute over several fractions, even when a sharp gradient is provided. Fractions identified to contain protein using the SDS gel were dialyzed into Pipes-magnesium buffer (10 mM Pipes, pH 7.0, 1 mM $MgCl_2$, 50% glycerol). The high glycerol in the dialysis buffer concentrates the protein five times and the typical yield is about 5 mg/L. Following dialysis the target protein was stored at $-20^{\circ}C$ and used in less than 1 week for kinetic assays and chromatography experiments.

Method for the Purification of alpha-crystallin

α -crystallin was purified from bovine lens using a modification of the procedure described by Stevens (FIG. 5). Alternatively α -crystallin was expressed and purified in *E. coli* using a procedure similar to that described for the bovine preparation above. Briefly 1 lens obtained from Animal Technologies (Tyler, TX) was stirred for 60 min at $4^{\circ}C$ with 5 ml of water and protease inhibitors (same as above). The protein was centrifuged at 13k rpm for 30 min and the supernatant was filtered through a $0.2\ \mu m$ filter prior to loading on a quaternary amine sepharose 5 ml HiTrap (catalog # 17-1154-01, lot # 276218; Amersham Pharmacia Biotech; Uppsala Sweden) column. The column was rinsed until the O.D. returned to baseline and the protein was eluted with a linear gradient of NaCl (50 mM-1 M). The fractions determined to contain α -crystallin were dialyzed for 18 hours against 10 mM Tris pH 8.0, 50% glycerol. 100 μl of 1 M glycine pH 2.5 is added to 1 ml of the dialyzed solution and then run on a 10 mm x 300 mm BioRad Macrorep SE 1000/40 gel filtration column. The selected fractions were quickly neutralized with 0.2 M Tris, pH 8.0 and the fractions containing the protease inhibition activity were pooled and dialyzed into 10 mM sodium bicarbonate buffer for coupling to resin (10 mM $NaHCO_3$ pH 8.0, 50% glycerol). The dialysis step is necessary because the elastase inhibition activity is strongly affected by ionic strength. The pooled fractions comprise a hetero-oligomer of α -A and α -B crystallin. Unlike the recombinant p26 which has a limited storage life the α -crystallin stored at $-20^{\circ}C$ was very stable. FIG.

5A shows the chromatograph of purified α -crystallin. FIG. 5B provides a digital image of an SDS PAGE gel of purified α -crystallin.

Use of alpha-A-crystallin as a Protease Affinity Chromatography Resin

5 The ability of α -crystallin or p26 coupled to CNBR Sepharose to inhibit elastase was examined by using a paranitroanilide substrate for elastase (Calbiochem, Cat# 324696, Lot #B27708). FIG. 6 provides a graph that shows the inhibition of elastase activity with α -crystallin. Elastase activity was measured using a para-nitroaniline substrate obtained from Calbiochem (La Jolla, CA). Assays were performed with a
10 Benchmark microplate reader (Bio-Rad). Elastase was purchased from either Sigma or Calbiochem. In a 100 μ l assay 50 μ g of peptide substrate, 1 μ g of elastase, and 50-100 μ g of either uncoupled p26, α -crystallin conjugated sepharose, BSA conjugated sepharose, or buffer (negative control) was used.

Findings indicate that α -crystallin sepharose inhibits up to 85% of the elastase in
15 protein extracts. The inventive pre-column filters can be regenerated with low pH solutions since α -crystallin is stable for a brief period in 0.1 M glycine pH 2.5. The lack of protease inhibition by p26 suggests that p26 and bovine lens α -crystallin are less similar than previously speculated.

In order to understand the salt dependance of inhibiting elastase by α -crystallin
20 sepharose, the elastase activity assays were repeated in the presence of various concentrations of sodium chloride. FIG. 7 is a graph that illustrates the NaCl dependency of α -crystallin in inhibiting elastase activity. One μ g of elastase was incubated with 5 μ l of α -crystallin conjugated sepharose in the presence of 0-200 mM NaCl. Increasing the NaCl concentration reduced the ability of α -crystallin to inhibit elastase activity. It was
25 determined that α -crystallin sepharose strongly inhibited elastase activity at low ionic strength (< 50 mM). At higher ionic strength (200 mM) the % inhibition of elastase decreased to 30%. Findings indicate that the optimal conditions for the pre-column filter resin is neutral pH (7-8) and low ionic strength.

For gel filtration chromatography a pre-column filter was placed in series with the
30 column during the entire run. After collecting the protease free fractions from the column run, the prepclean resin was taken offline and used for the next prep or if the

performance of the PrepClean resin decreased, then it could be cleaned with 0.1M glycine (pH 2.5). The low pH removed the bound proteases, thereby regenerating the column.

5 For ion exchange chromatography it is envisioned that the column would be placed in series with the resolving column as above. In this case, after the protein is loaded and washed in low salt, the pre-column filter would be removed just prior to running the salt gradient. Finally after extended use the pre-column filter could be rejuvenated with low pH as described above.

10 Modifications and variations can be made to the disclosed embodiments without departing from the subject and spirit of the invention as defined in the following claims. Such modifications and variations, as included within the scope of these claims, are meant to be considered part of the invention as described.